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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/591,632	06/09/2000	Susan Lindquist	27373/34978A	2820

7590 12/29/2005

Marshall O'Toole Gerstein  
Murray & Borun  
6300 Sears Tower  
233 South Wacker Drive  
Chicago, IL 60606-6402

EXAMINER

TURNER, SHARON L

ART UNIT PAPER NUMBER

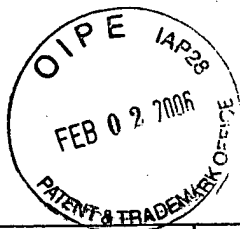
1649

DATE MAILED: 12/29/2005

Docketed:

1/29/06

Please find below and/or attached an Office communication concerning this application or proceeding.

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Alexandria, Virginia 22313-1450

APPLICATION NO/ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER
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ART UNIT	PAPER
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DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

**Commissioner for Patents**

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

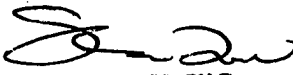
Any inquiry of a general nature or relating to the status of this general application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Papers relating to this application may be submitted to Technology Center 1600, Group 1640 by facsimile transmission. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). Should applicant wish to FAX a response, the current FAX number for Group 1600 is (703) 872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sharon L. Turner, Ph.D. whose telephone number is (571) 272-0894. The examiner can normally be reached on Monday-Thursday from 7:00 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Janet Andres can be reached at (571) 272-0867.

Sharon L. Turner, Ph.D.  
December 21, 2005

  
SHARON TURNER, PH.D.  
PRIMARY EXAMINER  
12-21-05

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/591,632B  
Source: IFW/6  
Date Processed by STIC: 12/8/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,  
Alexandria, VA 22314**

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

09/591,632B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ✓ PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) 15,17,40. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/591,632B

DATE: 12/08/2005  
TIME: 09:37:52

Input Set : A:\34978a.txt  
Output Set: N:\CRF4\12082005\I591632B.raw

4 <110> APPLICANT: Lindquist, Susan  
5 Li, Liming  
6 Ma, Jiyan  
7 Liu, Jia-Jia  
8 Sondheimer, Neal  
9 Scheibel, Thomas  
11 <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS  
12 AND METHODS COMPRISING SAME  
14 <130> FILE REFERENCE: 30554/34978A  
16 <140> CURRENT APPLICATION NUMBER: 09/591,632B  
17 <141> CURRENT FILING DATE: 2000-06-09  
19 <150> PRIOR APPLICATION NUMBER: US 06/138,833  
20 <151> PRIOR FILING DATE: 1999-06-09  
E--> 22 <160> NUMBER OF SEQ ID NOS: 65  
24 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

This version of PatentIn  
has bugs. (see item 6  
on Error Summary  
sheet)

Does Not Comply  
affected Diskette Needs

Suggestion: use a more  
recent version  
of PatentIn.

You can download  
PatentIn 3.3 (at no  
charge) from the USPTO  
website  
www.uspto.gov

09/59/632B 2

<210> 70 *last sequence in submitted file*  
<211> 286  
<212> PRT  
<213> Saccharomyces cerevisia

<400> 70

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala  
1 5 10 15

*see pp 3-4-5  
for more  
errors*

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/591,632B

DATE: 12/08/2005  
TIME: 09:37:54

Input Set : A:\34978a.txt  
Output Set: N:\CRF4\12082005\I591632B.raw

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:15,17,40

↓  
see p.4 for sample

This is due to Patent In 2.0 bug  
(see item 6 on Error  
summary  
sheet)



09/591,632B 4

<210> 15  
<211> 215  
<212> PRT  
<213> Artificial Sequence

↙ no 2207-2237 section

<400> 15  
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr  
1 5 10 15

09/89/632B 5

(from the end of sequence 3)

ggt gaa tga aggctgcttt aaaaacaaga aagaaagaag aaggaggaaa

1286

Gly Glu

(355) *Delete this, since no amino acid is shown under the stop*

agaagggttat aagggtatgt atataggcag aaaaaagga aaattaagtg caaatataaa 1346

Codon

caaaaatgtc atagaagtat ataatagttt tgaaatttct gttgcttcta ttatttcctt 1406

(tga)

gttaccctcaa ccacagaatt c

1427

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/09/591,632B**

**DATE: 12/08/2005**

**TIME: 09:37:54**

**Input Set : A:\34978a.txt**

**Output Set: N:\CRF4\12082005\I591632B.raw**

L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:803 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:803 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:803 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:803  
L:935 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:935 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:935 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:935  
L:2954 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39  
L:2962 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:40, <213>  
ORGANISM:Artificial Sequence  
L:2962 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:40, <213>  
ORGANISM:Artificial Sequence  
L:2962 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:2962  
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (65) Counted (70)

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